



## **RAW SEQUENCE LISTING ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/765,061

Source: OIPE

Date Processed by STIC: 8/15/2001

# 7 1/2

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/765,061

OIPE

DATE: 08/15/2001  
TIME: 11:44:00

INPUT SET: S36601.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply  
Corrected Diskette Needed

*use upper-case  
letters for headings*

*insert  
these  
mandatory  
headings  
and responses  
for a U.S.  
case*

## GENERAL INFORMATION: SEQUENCE LISTING

(1) General Information

(iii) NUMBER OF SEQUENCES: 1

78

(p.13)

(i) APPLICANT:  
(ii) TITLE OF INVENTION:

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:  
(B) STREET:  
(C) CITY:  
(D) STATE:  
(E) COUNTRY:  
(F) ZIP:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6749 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic) human

(ix) FEATURE:

(A) NAME/KEY: AIPL1 gene

(B) LOCATION: 17p13.1

(D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

19 ggccctcccaa agtgctggat tacaggcggtg agtcaccgcg cctgggtcccc tgtcttcttt 60  
20 aagaaagctc agcggacctt tttccttctt ggggtggaac aaaaagccaa atctagcaca 120  
21 accctgggca ggggcccgaga atcactggaa gcaaagggtg atgggatagg aggcgaggct 180  
22 gcctgtggac cacaggcccg gcccgagtgg ctctgatgag aagccggggc gcctagggtca 240  
23 ccgccccac cgtctgccct tccccccact cctcctggct gggtaaatcc cagagtctca 300  
24 gccgcctaag tgtcttcccc ggaggtgaga ttatctccgc ctgtgctgga cacctccctt 360  
25 tctcctgcag ccatggatgc cgctctgctc ctgaacgtgg aaggggtcaa gaaaaccatt 420  
26 ctgcacgggg gcacgggcga gctcccaaac ttcatcaccg gatcccgagt gagtggggcc 480  
27 cctccggagc agacagggtc cccacagca gctttcaaca ttccagggtg gccccaaggc 540  
28 actgtaaaac gctttcagct gtgccaaaaa aacagccagg cagccccagc ctgtggcctc 600  
29 cggggagctc ccagcggtta cccattcagg gggcattttt ggtactttgc agattcaact 660  
30 ttagcatggg ctgaggggaa gggttttttg gaattttctg gggccctaaa tgttgagtga 720  
31 gaagaaagg agtccgagga gtcttggtat ttgtcccaa atgtctgtta ggcttccctg 780  
32 gactgaaggg tgcgtctgtg gctacagaat tcgggctttg gccaggcgag gcggctcccg 840  
33 cctgtaatcc cagcactttg ggaggccaag atgggcagat catgagggtca agagttcgag 900  
34 accagcctga ccaacatgtg aaaccccatc tctactgaaa atacaaaaat tagccagatg 960  
35 tgctgtggcg cctgtaatcc cagttcagat actcaggaga cttgaggcag gagaatcact 1020  
36 tgagcccagg aggtggaggt tgcagtgagc cgagatcata ccactgcact ccaacctggg 1080  
37 caacagagtg agactctgtc tcagaaaaaa aaaaaaaa aagaactcgg gcttacttga 1140  
38 ggaaggattt ctggacgcac agggctgtgg ggagtgaat ggggtctgta gggaggggtg 1200  
39 ggtccctcct ccctgggggg tgcaggcagg gtggagggtc tccaggggtc tgaggcatct 1260

6689 (p.3)

*see  
pp 1-14*

*For bases,*

*use  
upper-case  
letters  
when using  
old sequence  
Bank  
format*

*FYI: all U.S. cases filed on or after July 1, 1998, and which  
cannot claim a prior application filed before July 1, 1998,  
need to be in new sequence Bank format.*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/765,061DATE: 08/15/2001  
TIME: 11:44:01

INPUT SET: S36601.raw

40	gatggggtga	actgagtga	ctgaccctgg	ggacagccct	gggtgtcggt	ggcaaggggg	1320
41	tggcttctgc	cgggccttga	acagtgtgtc	tagagcagag	tgcaccgtct	cggtgactag	1380
42	gtgatctttc	atttcgcac	catgaaatgt	gatgaggagc	ggacagtcac	tgacgacagt	1440
43	cggcaggtgg	gccagcccat	gcacatcatc	atcggaaca	tgttcaagct	cgaggtctgg	1500
44	gagatcctgc	ttacctccat	gcggtgtcac	gaggtggccg	agttctggtg	cgacaccatc	1560
45	gtaagtaggc	cctgcgcgcc	tgtctcctgg	gactagtctt	ttctgggctc	acccaccgc	1620
46	tttgcggggc	tgtgtgttt	cgggaaagct	gggactcaag	cgaagctttg	caaagccagt	1680
47	cctgcaact	tattccccac	cgtgtgcatg	tgaagatgga	gggaacaagg	gctggaagg	1740
48	gtgacccatg	ctgtggctgg	ctggtgggga	gcagggctat	gaccagcagg	agtgaagtgg	1800
49	cccacttcac	agtcctcaca	tctgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	1860
50	tgtgtgtgtg	agagagagag	agagagagag	agagagnnnn	nnnnnntagc	cttaggactt	1920
51	attgcagaga	ccaacaccta	acaatgtaat	caggcagcca	gtgcaggaca	taaataagta	1980
52	aggcagtggt	ctttgggcca	caaaagcacg	ctcagcttgc	tggaaagccat	gggtgccgag	2040
53	ctgggggctg	ctgagtcagg	gccaaggggg	gccccctcct	gcagtaagct	ggttctgggg	2100
54	cctctccctc	ccttgggtcca	gctcttaatc	ccaacaggct	caacagccat	ctgcttgtct	2160
55	cttccataaa	gaggcagaag	gcatttcggg	ctaattcccg	ccggtggggc	gggcagggtg	2220
56	acctctgtct	ctgtgtgtgt	gacctggagg	cagagctgaa	ctgctgcata	gagtttcagc	2280
57	cccttcactt	cacatgttgc	atgtggggcc	agtgtgtggg	catctcagaa	gccggtccaa	2340
58	ggagatgggt	tctcagggag	cctagtgtgg	gaaactgagg	cccagcatac	atacagcagg	2400
59	cctcgctgag	gccgcacggc	ggatcttccc	agccctcctt	catcccaagg	gtggcaaaact	2460
60	cagctcccat	gctggctgaa	gctgtgatga	gccagatcta	tatctgcacc	atctcattta	2520
61	atccctacag	cagccctaata	atcgaacagg	agcaacccag	ggaactgagt	ttcagagaag	2580
62	tgcagagacc	tgggctcacc	gctaacctgc	agcacttgca	ggacaccaaa	gcgactctct	2640
63	tggaccctgg	agtcctgctc	cttctactgc	cccacactgc	ccttctgctg	agtcataggc	2700
64	tttgagagg	tcagggtttc	cctggggcag	agatgtgtta	cagtggacca	caagggccag	2760
65	aagaggcagc	cggaggctaa	cagcatatgg	cctctggagc	caggtttgaa	tcctggctgc	2820
66	gtcatttcct	agctgtgtga	ccttaagcaa	gttgcttgcg	tctctgggct	gtagtttccc	2880
67	catccgtaaa	atgggataat	agtgcctgcc	ttgaattgtc	ataaggattg	aaggggctca	2940
68	taacagtgtg	aagtgcctttg	cctggcacac	agttaaccac	agttagtatg	agtggtcatg	3000
69	tgaggggagca	ggattcctcc	caggaggggc	tctgagtggg	ggccttttat	ggcccaccta	3060
70	gctctgggca	ggtagcctgg	atgccatcca	tccgtttatc	cccacagcac	acgggggtct	3120
71	acccctacat	rtcccggagc	ctgaggcaga	tggccaggag	caaggacccc	acagagtggc	3180
72	acgtgcacac	gtgcgggctg	gccaacatgt	tcgcctacca	cacgctgggc	tacaggagacc	3240
73	tggacgagct	gcagaaggag	cctcagcctc	tgggtctttgt	gatcgagctg	ctgcagggtg	3300
74	ggctgggggt	ggcagggtctg	gagggtgtgt	ccagcactgg	agagggacag	cgggcatcat	3360
75	gggcaccccc	acccactgg	ccactggaca	gtgccctgtt	tctgtttaga	taatacgaga	3420
76	gggttcataa	gccatgggag	aatacgaatt	tgaaaaaaaaa	gtcctctgat	ttttccacaa	3480
77	gaaaagtcct	ttggtgctgg	gcatggtggc	ccacgcctgt	aatcctagca	ctttggggagg	3540
78	ccgaggggggt	tggatcacct	gaggtcagga	gttcgaagac	cagcctggcc	aacatggtaa	3600
79	aaccccgctct	ctattaaaaa	cacaaaaatt	aaccgggtgt	ggtggtgcat	gcctgtaatc	3660
80	aatcccagct	acttgggaat	ttgaggcatg	agaattgctt	gaacctggaa	gtggagggtg	3720
81	cagtgagcag	agatcatgtc	agtgcatttt	aacctgggtg	acagagtga	actccatgtc	3780
82	caaaaaaaag	aaaaaaaaaa	aaagtccact	tgggaaccagt	ttttaaaaaa	gtgattcatt	3840
83	ttcattgtgg	aggcatttta	tccacttcca	ctttcatttt	caggagtgtg	agattataac	3900
84	cgcctccttg	gttcctgtgg	tttgtgggtt	cagacttggg	tctctngtgg	cgggagaggc	3960
85	tgcattggaac	tccccacatc	ctcccaacca	ggagccccag	agtgattggc	agcgcgtgtt	4020
86	tgtggattgg	tgagagaggg	ttaggggccag	ggtcaagggtc	aggtcaggac	tcagcttatg	4080
87	gccaagactg	aggctcagcc	tgagagctat	gtgggtgaat	aaaataaaat	aagaactgtg	4140
88	tcaaccaagg	gccccctaca	ggcttgctgt	cacagttgtg	tgggtctgtg	actgcacaag	4200
89	gtgcaccggc	atctcctcca	aggtgctcat	tatagacatt	gtatattggg	atttcataaa	4260
90	tgagaagttt	ccagcagatg	gcaatagtgt	attgttctaa	caaaacgagt	attcgtgaca	4320
91	attttctgaa	tattagaagt	gaagtgtctt	gatgaacggg	caccttttcc	tagtttgcac	4380
92	aaagacattg	atttagggca	gggttttcgg	cgttgttgct	tctttccctt	gtctgtatgc	4440

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/765,061

DATE: 08/15/2001  
TIME: 11:44:01

INPUT SET: S36601.raw

```

93  acttgaccag caagcatgac ttcagggaga tgtgccacag ggtcctgttt ttcgggtctc 4500
94  tgatggggtg caggccccctg ggggtccctgc ctcactgacc tgcagctctg gggccagggtt 4560
95  gatgccccga gtgattacca gagggagacc tggaaacctga gcaatcatga gaagatgaag 4620
96  gcggtgccccg tcctccacgg agagggaaat cggctcttca agctgggcccg ctacgaggag 4680
97  gcctcttcca agtaccagga ggccatcatc tgcctaagga acctgcagac caaggtcaga 4740
98  ggccgctggc caggggtggg aagtggcgct gactctgggg ggccctgccc gtgccggcca 4800
99  ggggtgggcg ggggttgggc agctgcctga ggtcatggct gaccttctcc ctgggcagga 4860
100 gaagccatgg gaggtgcagt ggctgaagct ggagaagatg atcaatactc tgatcctcaa 4920
101 ctactgccag tgcctgctga agaaggagga gtactatgag gtgctggagc acaccagtga 4980
102 tattctccgg caccacccag gtgcgcgggg ctgcaggggc ggacagttag ggggcgccc 5040
103 gccagggcc acggagacac ctgccatagc cttcctggac ttttctttcc accccaccag 5100
104 ggcaccaaac cttgtctcca cccagccggg ctttccccgag tgtgtaactg aattgtgggt 5160
105 gatggatggg cagtgccttg cgcgggcgcg ctttattttt aatgtgtgtt tgaacactta 5220
106 cccaggaagc tcgccaagct tgtgatttca gcggaacggt aaacaggcgt ttaaaaagag 5280
107 gggcaatcaa tatagggaaa aatattatga tgtcgggtact agtactggtg ttgcgaggat 5340
108 atggcaccgc agtactagat tgacttaatg ctcgaatcgt gctcacagta aaaacatcca 5400
109 gccctggct catgcatcag gcacacgtcg tctgcgttta ttatctcatt taatcctcat 5460
110 aatcctcata atcaccatat gagggagggtg cagggaaagg ggcctgaagg ttatctaatt 5520
111 taggtagcgt ctataagaaa aataaaacaa agttatgaat ataaaattac tcacagggcc 5580
112 ttaaaaagga gaggaggagg tactgctatt atgatcatca tctccatctt acagttgagg 5640
113 aaaccgaggg atgggggata cagagaggtt aaggatcatg gcggggctga gggctttgga 5700
114 ggctggtagg tcccagctgg gctggggctg cctctgaggc tgggaaggga gctgtagctg 5760
115 gatgctccct gctccccaca ggcatcgtga aggcctacta cgtgcgtgcc cgggctcacg 5820
116 cagaggtgtg gaatgaggcc gaggccaagg cggacctcca gaaagtgtg gagctggagc 5880
117 cgtccatgca gaaggcgggtg cgcagggagc ttgaggctgc tggagaaccg catggcggag 5940
118 aacaggagga ggagcggctg cgctgccgga acatgctgag ccagggtgcc acgcagcctc 6000
119 ccgcagagcc acccacagag ccacccgcac agtcatccac agagccacct gcagagccac 6060
120 ccacagcacc atctgcagag ctgtccgcag ggccccctgc agagccagcc acagagccac 6120
121 ccccgctccc agggcactcg ctgcagcact gagccccctg agggccacag ccacccaggc 6180
122 agggagcaag tggcctggtc acttctggtt cgattgacca ggatcgtggt gtcacttttt 6240
123 aaaatttaaa attaatTTTT gaaatcaaa tcagacacac ccatggtaaa aaaaaaaa 6300
124 aaaacaatcc caagggtaca gaagagctta tgaataaaag tagttttctc ctctaccct 6360
125 ctcatctctt ccgtgccatg gttttaattg accctgtttt taattcttct ggtagttttc 6420
126 tctatttcca agtaatctgt ttaaatacgt ttctagattt taccatgt caatgacaaa 6480
127 tgaggatttg atgctctgat ctttctcat gcctgatacc cctccctgtc tccccatttt 6540
128 ggatagttac atttgggggt catctcggtg attttgttaa ctttacgcag gacacttaga 6600
129 gctctctaga atcccactga ctttagtggg gtcttgatgt aggggtgggca agccccgaca 6660
--> 130 ctggagctta gcctgagagg ggttcttgc
131

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6749

6689

```

334  (2) INFORMATION FOR SEQ ID NO:8:
335  (i) SEQUENCE CHARACTERISTICS:
--> 336  (A) LENGTH: 1129 bases
337  (B) TYPE: nucleic acid
338  (C) STRANDEDNESS: single
339  (D) TOPOLOGY: linear
340  (ii) MOLECULE TYPE: cDNA Squirrel monkey
341  (ix) FEATURE:
342  (A) NAME/KEY: AIPL1 gene
343  (B) LOCATION:
344  (D) OTHER INFORMATION: produces aryl-hydrocarbon
345  receptor interacting protein-like 1
346  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/765,061

DATE: 08/15/2001  
TIME: 11:44:01

INPUT SET: S36601.raw

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347
348 atggatgccg ctctgctcct gaacgtggaa ggggtcaaga agaccattct gcacggggggc 60
349 acgggcgagc tcccaaatTT catcaccgga tcccgaagtga tctttcattt ccgcaccatg 120
350 aaatgtgatg aggagcggac ggtgattgac gacagcaggg aggtggggcca gcccatgcac 180
351 atcatcatcg ggaacatggt caagctggag gtctggggaga tcctgctcac gtccatgcgg 240
352 gtgcgagagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg 300
353 tcccggagcc tgcggcagat ggcccaggcg aaggaccgga cggagtggca tgtgcacacg 360
354 tgcgggctgg ccaacatggt cgcctaccac acgctgggct acgaggacct ggatgagctg 420
355 cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcagggtga tgccccaagt 480
356 gattaccaga gggagacctg gaacctgagc aatcacgaga agatgaagggt ggtgcccgtc 540
357 ctccatggag aaggaaatag gctcttcaag ctggggcgct acgaggaggc ctcttccaag 600
358 taccaggagg ccatcatctg cctaaggaaac ctgcagacca aggagaaacc ctgggagggtg 660
359 cagtggctga agctggagaa gatgatcaat accctgatcc tcaactactg tcagtgtctg 720
360 ctgaagaagg aggagtacta cgaggctcctg gagcatacca gtgacattct ccggcaccac 780
361 ccaggcattg tgaaggccta ctatgtgcgc gcccgggctc acgcggagggt gtggaacgag 840
362 gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccgtccat gcagaaggcg 900
363 gtgcgcaggg agctgaggct gctggagaac cgcattggcg agaagcagga ggaggagcgg 960
364 ctgcgctgcc gcaacatgct gagccagggg gccacgtggt ccccgcgga gccacccgca 1020
365 gagccacctg cagagtcac cagagagcca cccgcagagc cacctgcaga gccacctgca 1080
--> 366 gagctaacct tgaccccggg gcaccacta cagcactga 1129 1119
367

```

```

913 (2) INFORMATION FOR SEQ ID NO:42:
914 (i) SEQUENCE CHARACTERISTICS:
--> 915 (A) LENGTH: 20 bases
916 (B) TYPE: nucleic acid
917 (C) STRANDEDNESS: single
918 (D) TOPOLOGY: linear
919 (ii) MOLECULE TYPE: DNA Primer
920 (ix) FEATURE:
921 (A) NAME/KEY: AIPL1 primer
922 (B) LOCATION:
923 (D) OTHER INFORMATION: 5' to 3' order
924 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
925 delete 5'-aaggaaaacattctgcacgg-3'
926 prime
927 markers and hyphens

```

```

928 (2) INFORMATION FOR SEQ ID NO:43:
929 (i) SEQUENCE CHARACTERISTICS:
--> 930 (A) LENGTH: 19 bases
931 (B) TYPE: nucleic acid
932 (C) STRANDEDNESS: single
933 (D) TOPOLOGY: linear
934 (ii) MOLECULE TYPE: DNA Primer
935 (ix) FEATURE:
936 (A) NAME/KEY: AIPL1 primer
937 (B) LOCATION:
938 (D) OTHER INFORMATION:
939 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
940
941 5'-tgcagctcgtccaggctcct-3'
942

```

20  
Rules group bases  
into 10's and  
insert one space  
between groups

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/765,061DATE: 08/15/2001  
TIME: 11:44:02

INPUT SET: S36601.raw

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943 (2) INFORMATION FOR SEQ ID NO:44:  
944 (i) SEQUENCE CHARACTERISTICS:  
--> 945 (A) LENGTH: 17 bases  
946 (B) TYPE: nucleic acid  
947 (C) STRANDEDNESS: single  
948 (D) TOPOLOGY: linear  
949 (ii) MOLECULE TYPE: Primer DNA  
950 (ix) FEATURE:  
951 (A ) NAME/KEY: AIPL1 primer  
952 (B) LOCATION:  
953 (D) OTHER INFORMATION:  
954 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:  
955  
956 5'-gacacctccctttcttc-3' 17  
957

---

958 (2) INFORMATION FOR SEQ ID NO:45:  
959 (i) SEQUENCE CHARACTERISTICS:  
--> 960 (A) LENGTH: 18 bases  
961 (B) TYPE: nucleic acid  
962 (C) STRANDEDNESS: single  
963 (D) TOPOLOGY: linear  
964 (ii) MOLECULE TYPE: Primer DNA (genomic) human  
965 (ix) FEATURE:  
966 (A ) NAME/KEY: AIPL1 primer  
967 (B) LOCATION:  
968 (D) OTHER INFORMATION:  
969 (xi) SEQUENCE DESCRIPTION: ~~SEQ ID NO:45:~~  
970  
971 5'-gctggggctgcctggctg-3' 18  
972

---

973 (2) INFORMATION FOR SEQ ID NO:46:  
974 (i) SEQUENCE CHARACTERISTICS:  
--> 975 (A) LENGTH: 20 bases  
976 (B) TYPE: nucleic acid  
977 (C) STRANDEDNESS: single  
978 (D) TOPOLOGY: linear  
979 (ii) MOLECULE TYPE: Primer DNA (genomic) human  
980 (ix) FEATURE:  
981 (A ) NAME/KEY: AIPL1 Primer  
982 (B) LOCATION:  
983 (D) OTHER INFORMATION:  
984 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:  
985  
986 5'-ccgagtgattaccagaggga-3' 20  
987

---

988 (2) INFORMATION FOR SEQ ID NO:47:  
989 (i) SEQUENCE CHARACTERISTICS:  
--> 990 (A) LENGTH: 20 bases  
991 (B) TYPE: nucleic acid

*next page*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/765,061DATE: 08/15/2001  
TIME: 11:44:02

INPUT SET: S36601.raw

992 (C) STRANDEDNESS: single  
993 (D) TOPOLOGY: linear  
994 (ii) MOLECULE TYPE: Primer DNA (genomic) human  
995 (ix) FEATURE:  
996 (A ) NAME/KEY: AIPL1 Primer  
997 (B) LOCATION:  
998 (D) OTHER INFORMATION:  
999 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:  
1000  
1001 5'-tgagctccagcacctcatag-3'  
1002 20

1003 (2) INFORMATION FOR SEQ ID NO:48:  
1004 (i) SEQUENCE CHARACTERISTICS:  
--> 1005 (A) LENGTH: 18 bases  
1006 (B) TYPE: nucleic acid  
1007 (C) STRANDEDNESS: single  
1008 (D) TOPOLOGY: linear  
1009 (ii) MOLECULE TYPE: Primer DNA (genomic) human  
1010 (ix) FEATURE:  
1011 (A ) NAME/KEY: AIPL1 primer  
1012 (B) LOCATION:  
1013 (D) OTHER INFORMATION:  
1014 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:  
1015 5'-acgcagagggtgtggaatg-3'  
1016 18  
1017

1018 (2) INFORMATION FOR SEQ ID NO:49:  
1019 (i) SEQUENCE CHARACTERISTICS:  
--> 1020 (A) LENGTH: 19 bases  
1021 (B) TYPE: nucleic acid  
1022 (C) STRANDEDNESS: single  
1023 (D) TOPOLOGY: linear  
1024 (ii) MOLECULE TYPE: Primer DNA (genomic) human  
1025 (ix) FEATURE:  
1026 (A ) NAME/KEY: AIPL1 Primer  
1027 (B) LOCATION:  
1028 (D) OTHER INFORMATION:  
1029 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:  
1030 5'-aaaaagtgaçacçacgatc-3'  
1031 19  
1032

1113 (2) INFORMATION FOR SEQ ID NO:55:  
1114 (i) SEQUENCE CHARACTERISTICS:  
--> 1115 (A) LENGTH: 6689 bases 35(p. 7)  
1116 (B) TYPE: nucleic acid  
1117 (C) STRANDEDNESS: single  
1118 (D) TOPOLOGY: linear  
1119 (ii) MOLECULE TYPE: cDNA  
1120 (ix) FEATURE:  
1121 (A ) NAME/KEY: AIPL1 gene exon/intron Acceptor

RAW SEQUENCE LISTING  
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1122 splice site  
1123 (B) LOCATION:  
1124 (D) OTHER INFORMATION:  
1125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
1126  
1127 cactgacctgcagctctggggccagGTTGATGCCC 35  
1128

1194 (2) INFORMATION FOR SEQ ID NO:60:  
1195 (i) SEQUENCE CHARACTERISTICS:  
--> 1196 (A) LENGTH: 18 bases  
1197 (B) TYPE: nucleic acid  
1198 (C) STRANDEDNESS: single  
1199 (D) TOPOLOGY: linear  
1200 (ii) MOLECULE TYPE: DNA Primer  
1201 (ix) FEATURE:  
1202 (A ) NAME/KEY: AIPL1 gene Exon 1 Primer  
1203 (B) LOCATION: 240  
1204 (D) OTHER INFORMATION:  
1205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:  
1206  
1207 5'-ggaçacçtçççttççç-3' 18  
1208

1209 (2) INFORMATION FOR SEQ ID NO:61:  
1210 (i) SEQUENCE CHARACTERISTICS:  
--> 1211 (A) LENGTH: 18 bases  
1212 (B) TYPE: nucleic acid  
1213 (C) STRANDEDNESS: single  
1214 (D) TOPOLOGY: linear  
1215 (ii) MOLECULE TYPE: DNA Primer  
1216 (ix) FEATURE:  
1217 (A ) NAME/KEY: AIPL1 gene Exon 1 Primer  
1218 (B) LOCATION: 240  
1219 (D) OTHER INFORMATION:  
1220 (xi) SEQUENCE DESCRIPTION: ~~SEQ ID NO:61:~~  
1221  
1222 5'-gctggggçtçççtgççç-3' 18  
1223

1224 (2) INFORMATION FOR SEQ ID NO:62:  
1225 (i) SEQUENCE CHARACTERISTICS:  
--> 1226 (A) LENGTH: 20 bases  
1227 (B) TYPE: nucleic acid  
1228 (C) STRANDEDNESS: single  
1229 (D) TOPOLOGY: linear  
1230 (ii) MOLECULE TYPE: DNA Primer  
1231 (ix) FEATURE:  
1232 (A ) NAME/KEY: AIPL1 gene Exon 2 Primer  
1233 (B) LOCATION: 297  
1234 (D) OTHER INFORMATION:  
1235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:  
1236

*next page*



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1237  
1238

5'-gggccttgaacagtgtgtct-3'

20

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1239 (2) INFORMATION FOR SEQ ID NO:63:  
1240 (i) SEQUENCE CHARACTERISTICS:  
--> 1241 (A) LENGTH: 19 bases  
1242 (B) TYPE: nucleic acid  
1243 (C) STRANDEDNESS: single  
1244 (D) TOPOLOGY: linear  
1245 (ii) MOLECULE TYPE: DNA Primer  
1246 (ix) FEATURE:  
1247 (A ) NAME/KEY: AIPL1 gene Exon 2 Primer  
1248 (B) LOCATION: 297  
1249 (D) OTHER INFORMATION:  
1250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  
1251  
1252 5'-tttcccgaacacacagcagc-3'  
1253

19

---

1254 (2) INFORMATION FOR SEQ ID NO:64:  
1255 (i) SEQUENCE CHARACTERISTICS:  
--> 1256 (A) LENGTH: 18 bases  
1257 (B) TYPE: nucleic acid  
1258 (C) STRANDEDNESS: single  
1259 (D) TOPOLOGY: linear  
1260 (ii) MOLECULE TYPE: DNA Primer  
1261 (ix) FEATURE:  
1262 (A ) NAME/KEY: AIPL1 gene Exon 3 Primer  
1263 (B) LOCATION: 364  
1264 (D) OTHER INFORMATION:  
1265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:  
1266  
1267 5'-agtgaggagcaggattc-3'  
1268

18

---

1269 (2) INFORMATION FOR SEQ ID NO:65:  
1270 (i) SEQUENCE CHARACTERISTICS:  
--> 1271 (A) LENGTH: 20 bases  
1272 (B) TYPE: nucleic acid  
1273 (C) STRANDEDNESS: single  
1274 (D) TOPOLOGY: linear  
1275 (ii) MOLECULE TYPE: DNA Primer  
1276 (ix) FEATURE:  
1277 (A ) NAME/KEY: AIPL1 gene Exon 3 Primer  
1278 (B) LOCATION: 364  
1279 (D) OTHER INFORMATION:  
1280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:  
1281  
1282 5'-tgcccatgatgcccgctgtc-3'  
1283

20

---

1284 (2) INFORMATION FOR SEQ ID NO:66:  
1285 (i) SEQUENCE CHARACTERISTICS:

next row

RAW SEQUENCE LISTING  
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INPUT SET: S36601.raw

--> 1286 (A) LENGTH: 18 bases  
1287 (B) TYPE: nucleic acid  
1288 (C) STRANDEDNESS: single  
1289 (D) TOPOLOGY: linear  
1290 (ii) MOLECULE TYPE: DNA Primer  
1291 (ix) FEATURE:  
1292 (A ) NAME/KEY: AIPL1 gene Exon 4 Primer  
1293 (B) LOCATION: 315  
1294 (D) OTHER INFORMATION:  
1295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:  
1296  
1297 5'-tttcgggtctctgatggg-3'  
1298

18

---

1299 (2) INFORMATION FOR SEQ ID NO:67:  
1300 (i) SEQUENCE CHARACTERISTICS:  
--> 1301 (A) LENGTH: 17 bases  
1302 (B) TYPE: nucleic acid  
1303 (C) STRANDEDNESS: single  
1304 (D) TOPOLOGY: linear  
1305 (ii) MOLECULE TYPE: DNA Primer  
1306 (ix) FEATURE:  
1307 (A ) NAME/KEY: AIPL1 gene Exon 4 Primer  
1308 (B) LOCATION: 315  
1309 (D) OTHER INFORMATION:  
1310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:  
1311  
1312 5'-gcaggctcccagagtc-3'  
1313

17

---

1314 (2) INFORMATION FOR SEQ ID NO:68:  
1315 (i) SEQUENCE CHARACTERISTICS:  
--> 1316 (A) LENGTH: 19 bases  
1317 (B) TYPE: nucleic acid  
1318 (C) STRANDEDNESS: single  
1319 (D) TOPOLOGY: linear  
1320 (ii) MOLECULE TYPE: DNA Primer  
1321 (ix) FEATURE:  
1322 (A ) NAME/KEY: AIPL1 gene Exon 5 Primer  
1323 (B) LOCATION: 279  
1324 (D) OTHER INFORMATION:  
1325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:  
1326  
1327 5'-gcagctgcctcaggatcatg-3'  
1328

19

---

1329 (2) INFORMATION FOR SEQ ID NO:69:  
1330 (i) SEQUENCE CHARACTERISTICS:  
--> 1331 (A) LENGTH: 18 bases  
1332 (B) TYPE: nucleic acid  
1333 (C) STRANDEDNESS: single  
1334 (D) TOPOLOGY: linear  
1335 (ii) MOLECULE TYPE: DNA Primer

*next row*

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INPUT SET: S36601.raw

1336 (ix) FEATURE:  
1337 (A ) NAME/KEY: AIPL1 gene Exon 5 Primer  
1338 (B) LOCATION: 279  
1339 (D) OTHER INFORMATION:  
1340 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:  
1341  
1342 5'-gtggggtggaaagaaaag-3'  
1343 18

1344 (2) INFORMATION FOR SEQ ID NO:70:  
1345 (i) SEQUENCE CHARACTERISTICS:  
--> 1346 (A) LENGTH: 18 bases  
1347 (B) TYPE: nucleic acid  
1348 (C) STRANDEDNESS: single  
1349 (D) TOPOLOGY: linear  
1350 (ii) MOLECULE TYPE: DNA Primer  
1351 (ix) FEATURE:  
1352 (A ) NAME/KEY: AIPL1 gene Exon 6 Primer  
1353 (B) LOCATION: 497  
1354 (D) OTHER INFORMATION:  
1355 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:  
1356  
1357 5'-ctgggaagggagctgtag-3'  
1358 18

1359 (2) INFORMATION FOR SEQ ID NO:71:  
1360 (i) SEQUENCE CHARACTERISTICS:  
--> 1361 (A) LENGTH: 19 bases  
1362 (B) TYPE: nucleic acid  
1363 (C) STRANDEDNESS: single  
1364 (D) TOPOLOGY: linear  
1365 (ii) MOLECULE TYPE: DNA Primer  
1366 (ix) FEATURE:  
1367 (A ) NAME/KEY: AIPL1 gene Exon 6 Primer  
1368 (B) LOCATION: 497  
1369 (D) OTHER INFORMATION:  
1370 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:  
1371  
1372 5'-aaaagtgcaccacgatcc-3'  
1373 19

1374 (2) INFORMATION FOR SEQ ID NO:72:  
1375 (i) SEQUENCE CHARACTERISTICS:  
1376 (A) LENGTH: 383 amino acids  
1377 (B) TYPE: amino acid  
1378 (D) TOPOLOGY: linear  
1379 (ii) MOLECULE TYPE: protein  
1380 (ix) FEATURE:  
1381 (A ) NAME/KEY: Human Aipl1  
1382 (B) LOCATION:  
1383 (D) OTHER INFORMATION:  
1384 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:  
1385

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/765,061

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TIME: 11:44:04

INPUT SET: S36601.raw

1386 Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr  
1387 1 5 10 15  
1388 Ile Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly  
1389 20 25 30  
1390 Ser Arg Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu  
1391 35 40 45  
1392 Arg Thr Val Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His  
1393 50 55 60  
1394 Ile Ile Ile Gly Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu  
1395 65 70 75  
1396 Leu Thr Ser Met Arg Val His Glu Val Ala Glu Phe Trp Cys Asp  
1397 80 85 90  
1398 Thr Ile His Thr Gly Val Tyr Pro Ile Leu Ser Arg Ser Leu Arg  
1399 95 100 105  
1400 Gln Met Ala Gln Gly Lys Asp Pro Thr Glu Trp His Val His Thr  
1401 110 115 120  
1402 Cys Gly Leu Ala Asn Met Phe Ala Tyr His Thr Leu Gly Tyr Glu  
1403 125 130 135  
1404 Asp Leu Asp Glu Leu Gln Lys Glu Pro Gln Pro Leu Val Phe Val  
1405 140 145 150  
1406 Ile Glu Leu Leu Gln Val Asp Ala Pro Ser Asp Tyr Gln Arg Glu  
1407 155 160 165  
1408 Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys Ala Val Pro Val  
1409 170 175 180  
1410 Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly Arg Tyr Glu  
1411 185 190 195  
1412 Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu Arg Asn  
1413 200 205 210  
1414 Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys Leu  
1415 215 220 225  
1416 Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
1417 230 235 240  
1418 Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp  
1419 245 250 255  
1420 Ile Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg  
1421 260 265 270  
1422 Ala Arg Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala  
1423 275 280 285  
1424 Asp Leu Gln Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala  
1425 290 295 300  
1426 Val Arg Arg Glu Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys  
1427 305 310 315  
--> 1428 Gln Glu Glu Glu Arg Leu (xxx) Cys Arg Asn Met Leu Ser Gln Gly  
1429 320 325 330  
1430 Ala Thr Gln Pro Pro Ala Glu Pro Pro Thr Glu Pro Pro Ala Gln  
1431 335 340 345  
1432 Ser Ser Thr Glu Pro Pro Ala Glu Pro Pro Thr Ala Pro Ser Ala  
1433 350 355 360  
1434 Glu Leu Ser Ala Gly Pro Pro Ala Glu Pro Ala Thr Glu Pro Pro  
1435 365 370 375  
1436 Pro Ser Pro Gly His Ser Leu Gln His  
1437 380 383  
1438

invalid -  
use Xaa  
and explain  
in  
(ix) FEATURE:  
section

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/765,061

DATE: 08/15/2001  
TIME: 11:44:04

INPUT SET: S36601.raw

```

1439      (2) INFORMATION FOR SEQ ID NO:73:
1440      (i) SEQUENCE CHARACTERISTICS:
--> 1441      (A) LENGTH: 369 amino acids  ) 384 (next page)
1442      (B) TYPE: amino acid
1443      (D) TOPOLOGY: linear
1444      (ii) MOLECULE TYPE: protein
1445      (ix) FEATURE:
1446      (A ) NAME/KEY: Chimpanzee Aipl1
1447      (B) LOCATION:
1448      (D) OTHER INFORMATION:
1449      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
1450
1451      Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr
1452      1          5          10          15
1453      Ile Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly
1454      20          25          30
1455      Ser Arg Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu
1456      35          40          45
1457      Arg Thr Val Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His
1458      50          55          60
1459      Ile Ile Ile Gly Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu
1460      65          70          75
1461      Leu Thr Ser Met Arg Val His Glu Val Ala Glu Phe Trp Cys Asp
1462      80          85          90
1463      Thr Ile His Thr Gly Val Tyr Pro Ile Leu Ser Arg Ser Leu Arg
1464      95          100         105
1465      Gln Met Ala Gln Gly Lys Asp Pro Thr Glu Trp His Val His Thr
1466      110         115         120
1467      Cys Gly Leu Ala Asn Met Phe Ala Tyr His Thr Leu Gly Tyr Glu
1468      125         130         135
1469      Asp Leu Asp Glu Leu Gln Lys Glu Pro Gln Pro Leu Val Phe Val
1470      140         145         150
1471      Ile Glu Leu Leu Gln Val Asp Ala Pro Ser Asp Tyr Gln Arg Glu
1472      155         160         165
1473      Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys Ala Val Pro Val
1474      170         175         180
1475      Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly Arg Tyr Glu
1476      185         190         195
1477      Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu Arg Asn
1478      200         205         210
1479      Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys Leu
1480      215         220         225
1481      Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
1482      230         235         240
1483      Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp
1484      245         250         255
1485      Ile Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg
1486      260         265         270
1487      Ala Arg Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala
1488      275         280         285
1489      Asp Leu Arg Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala
1490      290         295         300

```

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/765,061

DATE: 08/15/2001  
TIME: 11:44:05

INPUT SET: S36601.raw

1491	Val Arg Arg Glu Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys	
1492		305 310 315
1493	Gln Glu Glu Glu Arg Leu Arg Cys Arg Asn Met Leu Ser Gln Gly	
1494		320 325 330
1495	Ala Thr Gln Pro Pro Ala Glu Pro Pro Thr Glu Pro Pro Ala Gln	
1496		335 340 345
1497	Ser Ser Thr Glu Pro Pro Ala Glu Pro Pro Pro Ala Pro Ser Ala	
1498		350 355 360
1499	Glu Leu Ser Ala Gly Pro Pro Ala Glu Thr Ala Thr Glu Pro Pro	
1500		365 370 375
1501	Pro Ser Pro Gly His Ser Leu Gln His	
1502		<del>365</del> <del>369</del>
1503		380

1748 (2) INFORMATION FOR SEQ ID NO:78:  
 1749 (i) SEQUENCE CHARACTERISTICS:  
 1750 (A) LENGTH: 372 amino acids  
 1751 (B) TYPE: amino acid  
 1752 (D) TOPOLOGY: linear  
 1753 (ii) MOLECULE TYPE: protein  
 1754 (ix) FEATURE:  
 1755 (A) NAME/KEY: Squirrel Monkey Aipl1  
 1756 (B) LOCATION:  
 1757 (D) OTHER INFORMATION:  
 1758 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:  
 1759

*Last sequence in file*

1760	Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr	
1761	1 5 10 15	
1762	Ile Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly	
1763	20 25 30	
1764	Ser Arg Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu	
1765	35 40 45	
1766	Arg Thr Val Ile Asp Asp Ser Arg Glu Val Gly Gln Pro Met His	
1767	50 55 60	
1768	Ile Ile Ile Gly Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu	
1769	65 70 75	
1770	Leu Thr Ser Met Arg Val Arg Glu Val Ala Glu Phe Trp Cys Asp	
1771	80 85 90	
1772	Thr Ile His Thr Gly Val Tyr Pro Ile Leu Ser Arg Ser Leu Arg	
1773	95 100 105	
1774	Gln Met Ala Gln Gly Lys Asp Pro Thr Glu Trp His Val His Thr	
1775	110 115 120	
1776	Cys Gly Leu Ala Asn Met Phe Ala Tyr His Thr Leu Gly Tyr Glu	
1777	125 130 135	
1778	Asp Leu Asp Glu Leu Gln Lys Glu Pro Gln Pro Leu Ile Phe Val	
1779	140 145 150	
1780	Ile Glu Leu Leu Gln Val Asp Ala Pro Ser Asp Tyr Gln Arg Glu	
1781	155 160 165	
1782	Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys Val Val Pro Val	
1783	170 175 180	
1784	Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly Arg Tyr Glu	
1785	185 190 195	
1786	Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu Arg Asn	

*see  
next page*

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PATENT APPLICATION US/09/765,061

DATE: 08/15/2001

TIME: 11:44:05

INPUT SET: S36601.raw

1787		200		205		210
1788	Leu Gln Thr Lys	Glu Lys Pro Trp Glu	Val Gln Trp Leu Lys	Leu		
1789		215		220		225
1790	Glu Lys Met Ile	Asn Thr Leu Ile Leu	Asn Tyr Cys Gln Cys	Leu		
1791		230		235		240
1792	Leu Lys Lys Glu	Glu Tyr Tyr Glu Val	Leu Glu His Thr Ser	Asp		
1793		245		250		255
1794	Ile Leu Arg His	His Pro Gly Ile Val	Lys Ala Tyr Tyr Val	Arg		
1795		260		265		270
1796	Ala Arg Ala His	Ala Glu Val Trp Asn	Glu Ala Glu Ala Lys	Ala		
1797		275		280		285
1798	Asp Leu Gln Lys	Val Leu Glu Leu Glu	Pro Ser Met Gln Lys	Ala		
1799		290		295		300
1800	Val Arg Arg Glu	Leu Arg Leu Leu Glu	Asn Arg Met Ala Glu	Lys		
1801		305		310		315
1802	Gln Glu Glu Glu	Arg Leu Arg Cys Arg	Asn Met Leu Ser Gln	Gly		
1803		320		325		330
1804	Ala Thr Trp Ser	Pro Ala Glu Pro Pro	Ala Glu Pro Pro Ala	Glu		
1805		335		340		345
1806	Ser Ser Thr Glu	Pro Pro Ala Glu Pro	Pro Ala Glu Pro Pro	Ala		
1807		350		355		360
1808	Glu Leu Thr Leu	Thr Pro Gly His Pro	Leu Gln His			
1809		365		370		
1810						

number the amino acids  
under every 5  
amino acids

# SEQUENCE VERIFICATION REPORT

## PATENT APPLICATION US/09/765,061

DATE: 08/15/2001  
TIME: 11:44:05

INPUT SET: S36601.raw

Line	Error	Original Text
4	Number of Sequences (1) Doesn't Equal Actual Count (78)	(iii) NUMBER OF SEQUENCES: 1
7	Entered (6749) and Calc. Seq. Length (6689) differ	(A) LENGTH: 6749 bases
130	# of Sequences for line conflicts w/ running total	ctggagctta gcctgagagg ggttcttgc
336	Entered (1129) and Calc. Seq. Length (1119) differ	(A) LENGTH: 1129 bases
366	# of Sequences for line conflicts w/ running total	gagctaacct tgaccccgagg gcaccacta cagcactga
915	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
930	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
945	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17 bases
960	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
975	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
990	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
1005	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1020	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1115	Entered (6689) and Calc. Seq. Length (35) differ	(A) LENGTH: 6689 bases
1196	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1211	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1226	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
1241	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1256	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1271	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH: 20 bases
1286	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1301	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17 bases
1316	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1331	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1346	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH: 18 bases
1361	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH: 19 bases
1428	Wrong Amino Acid Designator	Gln Glu Glu Glu Arg Leu Xxx Cys Arg Asn Met Leu Ser G
1441	Entered (369) and Calc. Seq. Length (384) differ	(A) LENGTH: 369 amino acids



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**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/765,061**

DATE: 08/15/2001  
TIME: 11:44:05

*INPUT SET: S36601.raw*

APPLICANT  
TITLE OF INVENTION  
ADDRESSEE  
STREET  
CITY  
STATE  
COUNTRY  
ZIP  
CORRESPONDENCE ADDRESS  
MEDIUM TYPE  
COMPUTER  
OPERATING SYSTEM  
SOFTWARE  
COMPUTER READABLE FORM  
APPLICATION NUMBER  
FILING DATE  
CLASSIFICATION  
CURRENT APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE  
PRIOR APPLICATION DATA